

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga
Yue, Henry
Corley, Neil C.
Shah, Purvi
- (ii) TITLE OF THE INVENTION: HUMAN NUCLEOLIN-LIKE PROTEIN
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0451 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-855-0555
 - (B) TELEFAX: 650-845-4166
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 545 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: TLYMNOT05
 - (B) CLONE: 2809795
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ala	Thr	Glu	His	Val	Asn	Gly	Asn	Gly	Thr	Glu	Glu	Pro	Met	Asp
1				5				10						15	
Thr	Thr	Ser	Ala	Val	Ile	His	Ser	Glu	Asn	Phe	Gln	Thr	Leu	Leu	Asp
		20						25					30		
Ala	Gly	Leu	Pro	Gln	Lys	Val	Ala	Glu	Lys	Leu	Asp	Glu	Ile	Tyr	Val
		35					40					45			
Ala	Gly	Leu	Val	Ala	His	Ser	Asp	Leu	Asp	Glu	Arg	Ala	Ile	Glu	Ala
		50				55				60					
Leu	Lys	Glu	Phe	Asn	Glu	Asp	Gly	Ala	Leu	Ala	Val	Leu	Gln	Gln	Phe
65				70					75					80	
Lys	Asp	Ser	Asp	Leu	Ser	His	Val	Gln	Asn	Lys	Ser	Ala	Phe	Leu	Cys
				85				90					95		
Gly	Val	Met	Lys	Thr	Tyr	Arg	Gln	Arg	Glu	Lys	Gln	Gly	Thr	Lys	Val
			100				105					110			
Ala	Asp	Ser	Ser	Lys	Gly	Pro	Asp	Glu	Ala	Lys	Ile	Lys	Ala	Leu	Leu
		115				120						125			
Glu	Arg	Thr	Gly	Tyr	Thr	Leu	Asp	Val	Thr	Thr	Gly	Gln	Arg	Lys	Tyr
		130				135					140				
Gly	Gly	Pro	Pro	Pro	Asp	Ser	Val	Tyr	Ser	Gly	Gln	Gln	Pro	Ser	Val
145					150					155					160
Gly	Thr	Glu	Ile	Phe	Val	Gly	Lys	Ile	Pro	Arg	Asp	Leu	Phe	Glu	Asp
				165					170					175	
Glu	Leu	Val	Pro	Leu	Phe	Glu	Lys	Ala	Gly	Pro	Ile	Trp	Asp	Leu	Arg
			180					185					190		
Leu	Met	Met	Asp	Pro	Leu	Thr	Gly	Leu	Asn	Arg	Gly	Tyr	Ala	Phe	Val
		195				200						205			
Thr	Phe	Cys	Thr	Lys	Glu	Ala	Ala	Gln	Glu	Ala	Val	Lys	Leu	Tyr	Asn
		210				215					220				
Asn	His	Glu	Ile	Arg	Ser	Gly	Lys	His	Ile	Gly	Val	Cys	Ile	Ser	Val
225					230					235					240
Ala	Asn	Asn	Arg	Leu	Phe	Val	Gly	Ser	Ile	Pro	Lys	Ser	Lys	Thr	Lys
				245					250					255	
Glu	Gln	Ile	Leu	Glu	Glu	Phe	Ser	Lys	Val	Thr	Glu	Gly	Leu	Thr	Asp
			260					265					270		
Val	Ile	Leu	Tyr	His	Gln	Pro	Asp	Lys	Lys	Lys	Asn	Arg	Gly	Phe	
		275					280				285				
Cys	Phe	Leu	Glu	Tyr	Glu	Asp	His	Lys	Thr	Ala	Ala	Gln	Ala	Arg	Arg
		290				295				300					
Arg	Leu	Met	Ser	Gly	Lys	Val	Lys	Val	Trp	Gly	Asn	Val	Gly	Thr	Val
305					310					315					320
Glu	Trp	Ala	Asp	Pro	Ile	Glu	Asp	Pro	Asp	Pro	Glu	Val	Met	Ala	Lys
				325					330					335	
Val	Lys	Val	Leu	Phe	Val	Arg	Asn	Leu	Ala	Asn	Thr	Val	Thr	Glu	Glu
			340					345					350		
Ile	Leu	Glu	Lys	Ala	Phe	Ser	Gln	Phe	Gly	Lys	Leu	Glu	Arg	Val	Lys
		355					360					365			
Lys	Leu	Lys	Asp	Tyr	Ala	Phe	Ile	His	Phe	Asp	Glu	Arg	Asp	Gly	Ala
		370				375				380					
Val	Lys	Ala	Met	Glu	Glu	Met	Asn	Gly	Lys	Asp	Leu	Glu	Gly	Glu	Asn
385					390					395					400
Ile	Glu	Ile	Val	Phe	Ala	Lys	Pro	Pro	Asp	Gln	Lys	Arg	Lys	Glu	Arg
				405					410					415	
Lys	Ala	Gln	Arg	Gln	Ala	Ala	Lys	Asn	Gln	Met	Tyr	Asp	Asp	Tyr	Tyr
				420				425					430		
Tyr	Tyr	Gly	Pro	Pro	His	Met	Pro	Pro	Pro	Thr	Arg	Gly	Arg	Gly	Arg
		435					440					445			
Gly	Gly	Arg	Gly	Gly	Tyr	Gly	Tyr	Pro	Pro	Asp	Tyr	Tyr	Gly	Tyr	Glu
		450				455					460				

Asp Tyr Tyr Asp Tyr Tyr Gly Tyr Asp Tyr His Asn Tyr Arg Gly Gly
 465 470 475 480
 Tyr Glu Asp Pro Tyr Tyr Gly Tyr Glu Asp Phe Gln Val Gly Ala Arg
 485 490 495
 Gly Arg Gly Gly Arg Gly Ala Arg Gly Ala Ala Pro Ser Arg Gly Arg
 500 505 510
 Gly Ala Ala Pro Pro Arg Gly Arg Ala Gly Tyr Ser Gln Arg Gly Gly
 515 520 525
 Pro Gly Ser Ala Arg Gly Val Arg Ala Gly Lys Arg Gly Arg Gly Arg
 530 535 540
 Ser
 545

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2079 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TLYMNOT05
 (B) CLONE: 2809795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGCGCGCGC	GCGCACCGGG	AGCGCGCTCG	GAGGCGAGTG	GAAC TGGATC	GGGTTTGCTG	60
CCAGCGGCGT	GAGCTTCGGC	CGGCATTTTA	CAACAGCTCC	ACTCGCGCCG	GACACAGGGA	120
GCAGCGAGCA	CGCGTTTCCC	GCAACCCGAT	ACCATCGGAC	AGGATTTCTC	CGCCTCAGCC	180
CAACGGGGAG	ATCTCTGGAA	ACATGGCTAC	AGAACATGTT	AATGGAAATG	GTA CTGAAGA	240
GCCCATGGAT	ACTACTTCTG	CAGTTATCCA	TTCAGAAAAT	TTTCAGACAT	TGCTTGATGC	300
TGGTTTACCA	CAGAAAGTTG	CTGAAAAACT	AGATGAAATT	TACGTTGCAG	GGCTAGTTGC	360
ACATAGTGAT	TTAGATGAAA	GAGCTATTGA	AGCTTTAAAA	GAATTC AATG	AAGACGGTGC	420
ATTGGCAGTT	CTTCAACAGT	TTAAAGACAG	TGATCTCTCT	CATGTT CAGA	ACAAAAAGTGC	480
CTTTTTATGT	GGAGTCATGA	AGACTTACAG	GCAGAGAGAA	AAACAAGGGA	CCAAAAGTAGC	540
AGATTCTAGT	AAAGGACCAG	ATGAGGCAAA	AATTAAGGCA	CTCTTG GAAA	GAACAGGCTA	600
CACACTTGAT	GTGACCACTG	GACAGAGGAA	GTATGGAGGA	CCACCTCCAG	ATTCCGTTTA	660
TTCAGGTCAG	CAGCCTTCTG	TTGGCACTGA	GATATTTGTG	GGAAAGATCC	CAAGAGATCT	720
ATTTGAGGAT	GAAC TTGTTT	CATTATTTGA	GAAAGCTGGA	CCTATATGGG	ATCTTCGTCT	780
AATGATGGAT	CCACTCACTG	GTCTCAATAG	AGGTTATGCG	TTTGTC ACTT	TTGTACAAA	840
AGAAGCAGCT	CAGGAGGCTG	TTAAACTGTA	TAATAATCAT	GAAATTCGTT	CTGGAAAACA	900
TATTGGTGTC	TGCATCTCAG	TTGCCAACAA	TAGGCTTTTT	GTGGGCTCTA	TTCC TAAGAG	960
TAAAACCAAG	GAACAGATTC	TTGAAGAATT	TAGCAAAGTA	ACAGAGGGTC	TTACAGACGT	1020
CATTTTATAC	CACCAACCGG	ATGACAAGAA	AAAAAACAGA	GGCTTTTGCT	TTCTTGAATA	1080
TGAAGATCAC	AAAACAGCTG	CCCAGGCAAG	GCGTAGGTTA	ATGAGTG GTA	AAGTCAAGGT	1140
CTGGGGGAAT	GTTGGAAC TG	TTGAATGGGC	TGATCCTATA	GAAGATCC TG	ATCCTGAGGT	1200
TATGGCAAAG	GTAAAAGTGC	TGTTTG TACG	CAACCTTGCC	AATACTGTAA	CAGAAGAGAT	1260
TTTAGAAAAG	GCATTTAGTC	AGTTTGGGAA	ACTGGAACGA	GTGAAGAAGT	TAAAAGATTA	1320
TGCGTTCATT	CATTTTGATG	AGCGAGATGG	TGCTGTCAAG	GCTATGGAAG	AAATGAATGG	1380
CAAGACTTGG	GAGGGAGAAA	ATATTGAAAT	TGTTTTTGCC	AAGCCACCAG	ATCAGAAAAG	1440
GAAAGAAAGA	AAAGCTCAGA	GGCAAGCAGC	AAAAAATCAA	ATGTATGACG	ATTACTACTA	1500
TTATGGTCCA	CCTCATATGC	CCCCCCAAC	AAGAGGTCGA	GGGCGTGGAG	G TAGAGGTGG	1560
TTATGGATAT	CCTCCAGATT	ATTATGGATA	TGAAGATTAT	TATGATTATT	ATGGTTATGA	1620
TTACCATAAC	TATCGTGGTG	GATATGAAGA	TCCATACTAT	GGTTATGAAG	ATTTTCAAGT	1680
TGGAGCTAGA	GGAAGGGGTG	G TAGAGGAGC	AAGGGGTGCT	GCTCCATCCA	GAGGTCGTGG	1740
GGCTGCTCCT	CCCCGCGGTA	GAGCCGGTTA	TTACAGAGA	GGAGGTCCTG	GATCAGCAAG	1800
AGGCGTTCGA	GCAGGGAAAA	GGGGTCGAGG	CCGGTCCTGA	CCTGTTACAA	TGAAGACTGA	1860
CTTGCTATGT	GGGATTACAC	CAGAAGCTTG	CAGTGGAGTA	ATGGTAAGGA	AATCAAGCAA	1920

CCTTAAATAT	GTCGGCTGTA	TAGGAGCATA	TTCTATTGCA	GAAGACCTTC	CTATGAAGAT	1980
CATGGAATCA	AATACGGGAC	ATTGAACTAA	TACTTGGACT	TTGATATGAA	TTTCTTTAAC	2040
AATTTTCTCT	GCAGTGCAAG	TTATTAAACT	AAAGCTACT			2079

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 128842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Val	Lys	Leu	Ala	Lys	Ala	Gly	Lys	Thr	His	Gly	Glu	Ala	Lys	Lys	1	5	10	15
Met	Ala	Pro	Pro	Pro	Lys	Glu	Val	Glu	Glu	Asp	Ser	Glu	Asp	Glu	Glu	20	25	30	
Met	Ser	Glu	Glu	Glu	Asp	Asp	Ser	Ser	Gly	Glu	Glu	Val	Val	Ile	Pro	35	40	45	
Gln	Lys	Lys	Gly	Lys	Lys	Ala	Thr	Ala	Thr	Pro	Ala	Lys	Lys	Val	Val	50	55	60	
Val	Ser	Gln	Thr	Lys	Lys	Val	Ala	Val	Pro	Thr	Pro	Ala	Lys	Lys	Ala	65	70	75	80
Ala	Val	Thr	Pro	Gly	Lys	Lys	Ala	Ala	Ala	Thr	Pro	Ala	Lys	Lys	Ala	85	90	95	
Val	Thr	Pro	Ala	Lys	Ala	Val	Ala	Thr	Pro	Gly	Lys	Lys	Gly	Ala	Thr	100	105	110	
Gln	Ala	Lys	Ala	Leu	Val	Ala	Thr	Pro	Gly	Lys	Lys	Gly	Ala	Val	Thr	115	120	125	
Pro	Ala	Lys	Gly	Ala	Lys	Asn	Gly	Lys	Asn	Ala	Lys	Lys	Glu	Asp	Ser	130	135	140	
Asp	Glu	Asp	Glu	Asp	Asp	Asp	Asp	Asp	Glu	Asp	Asp	Ser	Asp	Glu	Asp	145	150	155	160
Glu	Glu	Asp	Glu	Glu	Glu	Asp	Glu	Phe	Glu	Pro	Pro	Val	Val	Lys	Gly	165	170	175	
Lys	Gln	Gly	Lys	Val	Ala	Ala	Ala	Ala	Pro	Ala	Ser	Glu	Asp	Glu	Asp	180	185	190	
Glu	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Asp	195	200	205	
Asp	Ser	Glu	Glu	Glu	Glu	Ala	Met	Glu	Ile	Thr	Pro	Ala	Lys	Gly	Lys	210	215	220	
Lys	Ala	Pro	Ala	Lys	Val	Val	Pro	Val	Lys	Ala	Lys	Asn	Val	Ala	Glu	225	230	235	240
Glu	Asp	Asp	Asp	Asp	Glu	Glu	Glu	Asp	Glu	Asp	Glu	Glu	Glu	Asp	Glu	245	250	255	
Glu	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	260	265	270	
Pro	Val	Lys	Pro	Ala	Pro	Gly	Lys	Arg	Lys	Lys	Glu	Met	Thr	Lys	Gln	275	280	285	
Lys	Glu	Val	Pro	Glu	Ala	Lys	Lys	Gln	Lys	Val	Glu	Gly	Ser	Glu	Ser	290	295	300	
Thr	Thr	Pro	Phe	Asn	Leu	Phe	Ile	Gly	Asn	Leu	Asn	Pro	Asn	Lys	Ser	305	310	315	320
Val	Ala	Glu	Leu	Lys	Val	Ala	Ile	Ser	Glu	Pro	Phe	Ala	Lys	Asn	Asp	325	330	335	

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Leu	Ala	Val	Val	Asp	Val	Arg	Thr	Gly	Thr	Asn	Arg	Lys	Phe	Gly	Tyr
			340					345					350		
Val	Asp	Phe	Glu	Ser	Ala	Glu	Asp	Leu	Glu	Lys	Ala	Leu	Glu	Leu	Thr
		355					360					365			
Gly	Leu	Lys	Val	Phe	Gly	Asn	Glu	Ile	Lys	Leu	Glu	Lys	Pro	Lys	Gly
	370					375					380				
Arg	Asp	Ser	Lys	Lys	Val	Arg	Ala	Ala	Arg	Thr	Leu	Leu	Ala	Lys	Asn
385					390					395					400
Leu	Ser	Phe	Asn	Ile	Thr	Glu	Asp	Glu	Leu	Lys	Glu	Val	Phe	Glu	Asp
			405						410					415	
Ala	Leu	Glu	Ile	Arg	Leu	Val	Ser	Gln	Asp	Gly	Lys	Ser	Lys	Gly	Ile
			420					425					430		
Ala	Tyr	Ile	Glu	Phe	Lys	Ser	Glu	Ala	Asp	Ala	Glu	Lys	Asn	Leu	Glu
		435					440					445			
Glu	Lys	Gln	Gly	Ala	Glu	Ile	Asp	Gly	Arg	Ser	Val	Ser	Leu	Tyr	Tyr
	450					455					460				
Thr	Gly	Glu	Lys	Gly	Gln	Arg	Gln	Glu	Arg	Thr	Gly	Lys	Asn	Ser	Thr
465					470					475					480
Trp	Ser	Gly	Glu	Ser	Lys	Thr	Leu	Val	Leu	Ser	Asn	Leu	Ser	Tyr	Ser
			485					490						495	
Ala	Thr	Glu	Glu	Thr	Leu	Gln	Glu	Val	Phe	Glu	Lys	Ala	Thr	Phe	Ile
			500					505					510		
Lys	Val	Pro	Gln	Asn	Gln	Gln	Gly	Lys	Ser	Lys	Gly	Tyr	Ala	Phe	Ile
		515					520					525			
Glu	Phe	Ala	Ser	Phe	Glu	Asp	Ala	Lys	Glu	Ala	Leu	Asn	Ser	Cys	Asn
	530					535					540				
Lys	Met	Glu	Ile	Glu	Gly	Arg	Thr	Ile	Arg	Leu	Glu	Leu	Gln	Gly	Pro
545					550					555					560
Arg	Gly	Ser	Pro	Asn	Ala	Arg	Ser	Gln	Pro	Ser	Lys	Thr	Leu	Phe	Val
			565					570					575		
Lys	Gly	Leu	Ser	Glu	Asp	Thr	Thr	Glu	Glu	Thr	Leu	Lys	Glu	Ser	Phe
			580					585					590		
Glu	Gly	Ser	Val	Arg	Ala	Arg	Ile	Val	Thr	Asp	Arg	Glu	Thr	Gly	Ser
		595					600					605			
Ser	Lys	Gly	Phe	Gly	Phe	Val	Asp	Phe	Asn	Ser	Glu	Glu	Asp	Ala	Lys
	610					615					620				
Ala	Ala	Lys	Glu	Ala	Met	Glu	Asp	Gly	Glu	Ile	Asp	Gly	Asn	Lys	Val
625					630					635					640
Thr	Leu	Asp	Trp	Ala	Lys	Pro	Lys	Gly	Glu	Gly	Gly	Phe	Gly	Gly	Arg
			645					650					655		
Gly	Gly	Gly	Arg	Gly	Gly	Phe	Gly	Gly	Arg	Gly	Gly	Gly	Arg	Gly	Gly
			660					665					670		
Gly	Arg	Gly	Gly	Phe	Gly	Gly	Arg	Gly	Arg	Gly	Gly	Phe	Gly	Gly	Arg
		675					680					685			
Gly	Gly	Phe	Arg	Gly	Gly	Arg	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Asp	Phe
	690					695					700				
Lys	Pro	Gln	Gly	Lys	Lys	Thr	Lys	Phe	Glu						
705					710										